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	ttg tcc gag atg gat atc cgg gtg cgg gcg ctg gag acc atc ctg acc			
	96			
5	Leu Ser Glu Met Asp Ile Arg Val Arg Ala Leu Glu Thr Ile Leu Thr	20	25	30
	gag aag ggc tat gtc gat ccg gcg gcg ctc gac cgg atc gtc gag gcg			
	144			
10	Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala	35	40	45
	ttc gag acc agg atc ggc ccg cat atc ggc gcc cgt atc gtg gca cgg			
	192			
15	Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg	50	55	60
	gct tgg gcc gac gcc gaa ttc aag cgg cgg ctg ctc gcc gac gcg acc			
	240			
20	Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr	65	70	75
				80
	gag gcg gcg aat tcg ctg ggt cat gcg agc ccg gtc ggc agc cat ctg			
	288			
25	Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu	85	90	95
	atc gcg gtc gag aac acg ccg cag acc cac aac ctc gtc gtc tgc act			
	336			
30	Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr	100	105	110
	ttg tgc tcg tgt tat ccg tgg gag gtg ctg gga ttg ccg ccg gtc tgg			
	384			
35	Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp	115	120	125
	tac aaa tcc gct gcc tac cgc tcg cgc gtg gtg atc gac ccc aag ggc			
	432			
40	Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly	130	135	140
	gtc ctc gcc gag ttc ggc ctg acc ctg cca ccg gag acc ggg atc cgc			
	480			
45	Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg	145	150	155
				160
	atc tgg gat tcg acc gcc gag acc cgg ttt ctg gtg gtg ccg atg cgg			
	528			
50	Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg	165	170	175
	ccc ccc ggc acc gca ggc tgg agc gag gaa cgg ctc gcc gaa ctc gtc			
	576			
55	Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val	180	185	190
	acc cgc gac agc atg atc ggc act ggt ctg gcc ggg gcg ccg cag gag			
	624			

Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu
 195 200 205

5 atg gcc tcg gca tga
 639
 Met Ala Ser Ala
 210

10 <210> 44
 <211> 212
 <212> PRT
 <213> Unknown

15 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M2K17
 <400> 44

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 1 5 10 15

25 Leu Ser Glu Met Asp Ile Arg Val Arg Ala Leu Glu Thr Ile Leu Thr
 20 25 30

30 Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala
 35 40 45

Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg
 50 55 60

35 Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr
 65 70 75 80

40 Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu
 85 90 95

45 Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr
 100 105 110

50 Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp
 115 120 125

Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly
 130 135 140

55 Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg
 145 150 155 160

Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg
165 170 175

5 Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val
180 185 190

10 Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu
195 200 205

Met Ala Ser Ala
210

15

<210> 45
<211> 696
<212> DNA
20 <213> Unknown

<220>
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25 <220>
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48
Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg
1 5 10 15

35 ctg cat gat cga gct ggc ggc gtt cga tca ttg cgc ggc aaa agg tct
96
Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser
20 25 30

40 cat cgc gcc gga tcg cat cct cgg ggc gct cgc gca tcc gtc gcc aca
144
His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr
35 40 45

45 ggg tgg ttc gtt ccg ttc tcg gcc agg ctc gcc cgg aaa ggc atc gct
192
Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala
50 55 60

50 cct ccg gcc gag atc gcc gag cgg atc gcc gtc acc gat cgc gca tca
240
Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser
65 70 75 80

55 ccg gca atg ggc gct cgc atg gtc gcc aag gcc tgg acc gat ccc gcc
288
Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala
85 90 95

ttc cgc acc ctg ctc ttg gaa gac gga acc cgc gcg gcg gaa tcg ctc
 336
 5 Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu
 100 105 110

ggc atc atg atg cgc ggc gcc ccg cct ctc ggt gtg ctg gag aat acg
 384
 10 Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr
 115 120 125

ccc gag att cat cac ctc gtc gtt tgc acg ctg tgc agt tgt tac ccg
 432
 15 Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro
 130 135 140

cgc gcg gtg ctg ggc tat ccg ccg ttc tgg ttc aaa tcc gcc gcc tac
 480
 20 Arg Ala Val Leu Gly Tyr Pro Pro Phe Trp Phe Lys Ser Ala Ala Tyr
 145 150 155 160

cgg gca cgt gcg gtg cgc gac ccg cgc ggt ctg atc gcc gaa tgg ggc
 528
 25 Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly
 165 170 175

acc atg ctg ccc gac gat gtc cgc gtg cga gtg gtg gac agt acg gcc
 576
 30 Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala
 180 185 190

gac tat cgc tgg atg gtt ctg ccg gtg cgg ccg gcc ggc act gcg ggc
 624
 35 Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly
 195 200 205

tgg gat gag gag cgc ctc gcc gca atc gta cgc gaa ggc gat atg atc
 672
 40 Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile
 210 215 220

ggg gtg acc atc cct cgt ctt taa
 696
 45 Gly Val Thr Ile Pro Arg Leu
 225 230

<210> 46
 <211> 231
 50 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M15aA6
 55 <400> 46

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 1 5 10 15

5 Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser
 20 25 30
 His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr
 35 40 45
 10 Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala
 50 55 60
 15 Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser
 65 70 75 80
 20 Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala
 85 90 95
 Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu
 100 105 110
 25 Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr
 115 120 125
 30 Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro
 130 135 140
 35 Arg Ala Val Leu Gly Tyr Pro Pro Phe Trp Phe Lys Ser Ala Ala Tyr
 145 150 155 160
 40 Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly
 165 170 175
 Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala
 180 185 190
 45 Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly
 195 200 205
 50 Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile
 210 215 220
 55 Gly Val Thr Ile Pro Arg Leu
 225 230

<211> 576
 <212> DNA
 <213> Unknown

5 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M23dA12

<220>
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 <223>

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 atg cag ttg cgc gtg cgg gcg ctg gaa acc gtt cta gcc gaa aag ggt
 15 48
 Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly
 1 5 10 15
 tat ctc gat ccc gcc gcg ctt gat gcg atg atc gaa gcc tac gag acg
 20 96
 Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr
 20 25 30
 cgg att ggg ccg cat aac ggc gcg cgc gtc gtc gcc aag gcc tgg tcc
 25 144
 Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser
 35 40 45
 gac gcc gca ttc aag cga gcg ctg gtc gag gat gcg acc aag gcc gtg
 30 192
 Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val
 50 55 60
 cag tcg ttc ggc gtg gtc aat cgc gtc ggc gat cac ctg atc gcg gtc
 35 240
 Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val
 65 70 75 80
 gag aac acg ccc acg ctg cac aac atc atc gtg tgc acg ttg tgc tcc
 40 288
 Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser
 85 90 95
 tgc tat ccg tgg gaa gtg ctc ggc ctg ccg ccg gtc tgg tac aaa tcg
 45 336
 Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser
 100 105 110
 gcg ccc tac cgc tcg cgc gcg gtc aac gac ccg cgc ggg gta ctc gcc
 50 384
 Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala
 115 120 125
 gat ttc ggc ctg aag ctg gcg ccg gat atg caa atc cgt gtc tgg gat
 55 432
 Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp
 130 135 140

tcg acc gcc gag acg cgc ttc atc gtg ttg ccg atg cgc ccg gcc gga
 480
 Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly
 145 150 155 160
 5
 acc gac ggc tgg agc gaa gaa aag ctc gcc gcg ctg gtg aca cgc gat
 528
 Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp
 165 170 175
 10
 tgc atg atc ggc acc ggc tta ccc aag caa ccc aac gag gtc acg taa
 576
 Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr
 180 185 190
 15
 <210> 48
 <211> 191
 <212> PRT
 20 <213> Unknown
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 25 <400> 48
 Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly
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 30
 Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr
 20 25 30
 35 Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser
 35 40 45
 40 Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val
 50 55 60
 45 Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val
 65 70 75 80
 Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser
 85 90 95
 50 Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser
 100 105 110
 55 Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala
 115 120 125
 Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp

130 135 140

5 Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly
145 150 155 160

10 Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp
165 170 175

15 Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr
180 185 190

20 <210> 49
<211> 624
<212> DNA
<213> Unknown

25 <220>
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<222> (1)..(624)
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48
Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu
1 5 10 15

35 tcg cag gcg gca ttg cgc gcg aag gcg atc gaa tcg ctg ctg gtc gaa
96
Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu
20 25 30

40 aag ggg ctg atc gcg acc gac gtg atc gat cgc gtg gta gca acg tac
144
Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr
35 40 45

45 gag aaa gaa gtc ggg ccg ctc aac ggc gct aaa gtc gtc gcg cgg gcc
192
Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala
50 55 60

50 tgg acc gat ccg gag tac cgc cgc aga ctg ctc aag aac ggc acg gcg
240
Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala
65 70 75 80

55 gcg att gcc gag ctg gga ttc ggc ggc ttg cag ggc gaa cac atg atg
288
Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met
85 90 95

gtc gtg gaa aac acg ccg tcc gta cat aac gtg atc tgt tgc acg cta
 336
 Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu
 100 105 110
 5
 tgc tca tgc tat ccg tgg ccg gtc ctg gga ctt ccg ccg agc tgg tac
 384
 Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr
 115 120 125
 10
 aag tcg ctg gcg tat cgt tcg cga atc gtg cgc gag ccg cgc gcc gtc
 432
 Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val
 130 135 140
 15
 ctc ggc gaa ttc ggc ctc gaa ttg ccc gaa acg gtg gaa gtc cgc gta
 480
 Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val
 145 150 155 160
 20
 tgg gat agc agt gct gag atg cgc tat ctc gtg ttg ccg gag cgt cca
 528
 Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro
 165 170 175
 25
 gcg gga acg acg gag ttg agc gaa gcg gaa ttg gct tca ttg atc acg
 576
 Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr
 180 185 190
 30
 cgc gat gcc ttg atc ggc gtg gcg aaa gtc gcg gcg cca agc cgc tag
 624
 Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg
 195 200 205
 35
 <210> 50
 <211> 207
 <212> PRT
 40 <213> Unknown
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 <223> Metagenome - alpha unit nitrile hydratase - M49bD9
 45 <400> 50
 Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu
 1 5 10 15
 50
 Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu
 20 25 30
 55
 Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr
 35 40 45
 Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala

50 55 60

5 Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala
65 70 75 80

10 Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met
85 90 95

Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu
100 105 110

15 Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr
115 120 125

20 Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val
130 135 140

25 Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val
145 150 155 160

30 Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro
165 170 175

Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr
180 185 190

35 Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg
195 200 205

40 <210> 51
<211> 600
<212> DNA
<213> Unknown

45 <220>
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50 <222> (1)..(600)
<223>

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48
Met Ser Asn Pro Arg Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg
1 5 10 15

gcc aag gcg ctc gca gaa gcg ctt tcg aag caa gga ctc gtg ccg gaa
 96
 Ala Lys Ala Leu Ala Glu Ala Leu Ser Lys Gln Gly Leu Val Pro Glu
 20 25 30
 5
 ggg ttc ctc gac cag gtc ggt tct cac gcc gcg gag gcg tgg agc ccg
 144
 Gly Phe Leu Asp Gln Val Gly Ser His Ala Ala Glu Ala Trp Ser Pro
 35 40 45
 10
 cga aac ggc gca cgg gtc gtg gcg cgg gcg tgg gtg gat ccc gag tac
 192
 Arg Asn Gly Ala Arg Val Val Ala Arg Ala Trp Val Asp Pro Glu Tyr
 50 55 60
 15
 cgg acg cgc ttg ctc gcc gac ggc acc gcc gcg tgc gcc gcg ctc ggc
 240
 Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala Ala Cys Ala Ala Leu Gly
 65 70 75 80
 20
 tac gcg gga ccg cag gga gag tac atc gtg gta ctc gaa gac acg ctg
 288
 Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val Val Leu Glu Asp Thr Leu
 85 90 95
 25
 gcc gtt cac aac gtg atc gtg tgt acg caa tgc tcg tgt act gcg tgg
 336
 Ala Val His Asn Val Ile Val Cys Thr Gln Cys Ser Cys Thr Ala Trp
 100 105 110
 30
 ccc gtg ctg ggg ctg ccg ccc gat tgg tac aag agt ccg gag tat cgc
 384
 Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser Pro Glu Tyr Arg
 115 120 125
 35
 gcc cgc gtc gtg cgg gag ccg cga cgg gtg ctt cgc gaa atg ggc ctc
 432
 Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg Glu Met Gly Leu
 130 135 140
 40
 gag cta tcc gag agc gtg acg atc cgc gtg tgg gat acg act gcg gaa
 480
 Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu
 145 150 155 160
 45
 acg cgc ttc ctg gtg ctg ccg ctt cgg ccg gcg gga acc gaa ggg tgg
 528
 Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp
 165 170 175
 50
 agc gcg gag cag ctc gcg tcg ctc gtc acg cgc gag gcg atg atc ggc
 576
 Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly
 180 185 190
 55
 gtg gcg cgg gtc gag gtg gtg tag
 600
 Val Ala Arg Val Glu Val Val
 195

5 <210> 52
 <211> 199
 <212> PRT
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 10 <220>
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 <400> 52

 15 Met Ser Asn Pro Arg Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg
 1 5 10 15

 Ala Lys Ala Leu Ala Glu Ala Leu Ser Lys Gln Gly Leu Val Pro Glu
 20 20 25 30

 20 Gly Phe Leu Asp Gln Val Gly Ser His Ala Ala Glu Ala Trp Ser Pro
 35 40 45

 25 Arg Asn Gly Ala Arg Val Val Ala Arg Ala Trp Val Asp Pro Glu Tyr
 50 55 60

 30 Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala Ala Cys Ala Ala Leu Gly
 65 70 75 80

 Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val Val Leu Glu Asp Thr Leu
 35 85 90 95

 Ala Val His Asn Val Ile Val Cys Thr Gln Cys Ser Cys Thr Ala Trp
 100 105 110

 40 Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser Pro Glu Tyr Arg
 115 120 125

 45 Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg Glu Met Gly Leu
 130 135 140

 50 Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu
 145 150 155 160

 Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp
 55 165 170 175

 Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly
 180 185 190

Val Ala Arg Val Glu Val Val
195

5
<210> 53
<211> 645
<212> DNA
<213> Unknown

10
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<223> Metagenome - alpha unit nitrile hydratase - M25A18

15
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<221> CDS
<222> (1)..(645)
<223>

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<400> 53
atg agc ggc acg cat cac cac gac cat gac cac gat cat gac cat gcc
48
Met Ser Gly Thr His His His Asp His Asp His Asp His Asp His Ala
1 5 10 15

25
cat ccg ggc gtc gcc aag gac gag aag gtc cac ggc tat tac caa ttg
96
His Pro Gly Val Ala Lys Asp Glu Lys Val His Gly Tyr Tyr Gln Leu
20 25 30

30
ctc ggc ctc gcc atc aaa gag ctg ctg atc gaa aaa ggc gtc atc acc
144
Leu Gly Leu Ala Ile Lys Glu Leu Ile Glu Lys Gly Val Ile Thr
35 40 45

35
gcc gcc gag gtg cgc caa gcg atc gag gcg cgc gac gcg atc acg ccg
192
Ala Ala Glu Val Arg Gln Ala Ile Glu Ala Arg Asp Ala Ile Thr Pro
50 55 60

40
tcg ctc ggc ggc aag gtg gtc gcg cgc gcc tgg acc gat ccg gcc tac
240
Ser Leu Gly Gly Lys Val Val Ala Arg Ala Trp Thr Asp Pro Ala Tyr
65 70 75 80

45
aag gcg cgg ctg atc gcc gat ccc gcc gcc gcc atg atg gag atg ggc
288
Lys Ala Arg Leu Ile Ala Asp Pro Ala Ala Ala Met Met Glu Met Gly
85 90 95

50
gtc gat ctc ggc ccc acc gga ctc gcc atc gcc gag aac acg ccg gag
336
Val Asp Leu Gly Pro Thr Gly Leu Ala Ile Ala Glu Asn Thr Pro Glu
100 105 110

55
gcg cac aac gtc atc gtc tgc acc ctg tgc tcg tgc tat ccg cgc gcc
384
Ala His Asn Val Ile Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ala
115 120 125

gtg ctc ggc ctg ccg ccc tcc tgg tac aag gac cgc gat tac cgg tcg
 432
 Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Asp Arg Asp Tyr Arg Ser
 130 135 140
 5 cgc gtg gtg cgc gag ccg cgc gcc gtg ctc aag gag ttc ggc acg gaa
 480
 Arg Val Val Arg Glu Pro Arg Ala Val Leu Lys Glu Phe Gly Thr Glu
 145 150 155 160
 10 ttg ccc gac gac gtc gac gtc cgc gtc cac gat tcg acc gcc gat ctg
 528
 Leu Pro Asp Asp Val Asp Val Arg Val His Asp Ser Thr Ala Asp Leu
 165 170 175
 15 cgc tat ctc gtg ctg ccg atg cgc ccg gcc ggc acc gag ggc atg agc
 576
 Arg Tyr Leu Val Leu Pro Met Arg Pro Ala Gly Thr Glu Gly Met Ser
 180 185 190
 20 gag gcg gag ctg gcc gag atc gtg acg cgc gac tgc atg atc ggc gtg
 624
 Glu Ala Glu Leu Ala Glu Ile Val Thr Arg Asp Cys Met Ile Gly Val
 195 200 205
 25 acg gtg ccg aaa gcg ccc taa
 645
 Thr Val Pro Lys Ala Pro
 210
 30 <210> 54
 <211> 214
 <212> PRT
 35 <213> Unknown
 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M25A18
 40 <400> 54
 Met Ser Gly Thr His His His Asp His Asp His Asp His Asp His Ala
 1 5 10 15
 45 His Pro Gly Val Ala Lys Asp Glu Lys Val His Gly Tyr Tyr Gln Leu
 20 25 30
 50 Leu Gly Leu Ala Ile Lys Glu Leu Leu Ile Glu Lys Gly Val Ile Thr
 35 40 45
 55 Ala Ala Glu Val Arg Gln Ala Ile Glu Ala Arg Asp Ala Ile Thr Pro
 50 55 60
 Ser Leu Gly Gly Lys Val Val Ala Arg Ala Trp Thr Asp Pro Ala Tyr
 65 70 75 80

5 Lys Ala Arg Leu Ile Ala Asp Pro Ala Ala Ala Met Met Glu Met Gly
 85 90 95
 Val Asp Leu Gly Pro Thr Gly Leu Ala Ile Ala Glu Asn Thr Pro Glu
 100 105 110
 10 Ala His Asn Val Ile Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ala
 115 120 125
 15 Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Asp Arg Asp Tyr Arg Ser
 130 135 140
 20 Arg Val Val Arg Glu Pro Arg Ala Val Leu Lys Glu Phe Gly Thr Glu
 145 150 155 160
 Leu Pro Asp Asp Val Asp Val Arg Val His Asp Ser Thr Ala Asp Leu
 165 170 175
 25 Arg Tyr Leu Val Leu Pro Met Arg Pro Ala Gly Thr Glu Gly Met Ser
 180 185 190
 30 Glu Ala Glu Leu Ala Glu Ile Val Thr Arg Asp Cys Met Ile Gly Val
 195 200 205
 35 Thr Val Pro Lys Ala Pro
 210
 40 <210> 55
 <211> 627
 <212> DNA
 <213> Unknown
 <220>
 45 <223> Metagenome - alpha unit nitrile hydratase
 <220>
 <221> CDS
 <222> (1)..(627)
 50 <223>
 <400> 55
 atg agc ggt cac cat cac gac cac gac cat gag cac gac aac cac ttc
 48
 55 Met Ser Gly His His His Asp His Asp His Glu His Asp Asn His Phe
 1 5 10 15
 acg ccg atc gaa gcg cgc gtg aag gcg ctg gaa tcg ctg ctg gtc gcc
 96

Thr Pro Ile Glu Ala Arg Val Lys Ala Leu Glu Ser Leu Leu Val Ala
 20 25 30
 5 aag ggc tat gtc gat ccc gcc gcg ctc gat gcg atc atc gac acc tat
 144
 Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Ala Ile Ile Asp Thr Tyr
 35 40 45
 10 gag acg aag atc ggc ccg cgc aac ggc gcc cgc gtc gtc gcc aag gcc
 192
 Glu Thr Lys Ile Gly Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala
 50 55 60
 15 tgg acc gat ccg gaa ttc gcg gcg cgg ctc aag cag gat ggc agc gcc
 240
 Trp Thr Asp Pro Glu Phe Ala Ala Arg Leu Lys Gln Asp Gly Ser Ala
 65 70 75 80
 20 gcc gtc gcc gaa ctc ggc tat ggc ggg cgt ggc gcc gag cat atc gtc
 288
 Ala Val Ala Glu Leu Gly Tyr Gly Gly Arg Gly Gly Glu His Ile Val
 85 90 95
 25 gcc tgt ttc aat acg ccc gaa gag cac aac ctg atc gtc tgc acg ctc
 336
 Ala Cys Phe Asn Thr Pro Glu Glu His Asn Leu Ile Val Cys Thr Leu
 100 105 110
 30 tgc tcg tgc tat ccc tgg ccg gtg ctc ggc ctg ccg ccg gtc tgg tac
 384
 Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Val Trp Tyr
 115 120 125
 35 aaa tcc ccg ccc tat cgc tcg aaa gcg gtg atc gac ccg cgc ggc gtg
 432
 Lys Ser Pro Pro Tyr Arg Ser Lys Ala Val Ile Asp Pro Arg Gly Val
 130 135 140
 40 ctg gcc gat ttc ggc gtg acc ctg ccg gag gga caa agg atc cgc gtc
 480
 Leu Ala Asp Phe Gly Val Thr Leu Pro Glu Gly Gln Arg Ile Arg Val
 145 150 155 160
 45 tgg gat tcc acc gcc gaa acc cgc ttc att gtc atc ccc ctg cgc ccg
 528
 Trp Asp Ser Thr Ala Glu Thr Arg Phe Ile Val Ile Pro Leu Arg Pro
 165 170 175
 50 gcc ggg acg gaa ggc tgg tcg gaa gaa cag ctg gcg gcg atc gtg acg
 576
 Ala Gly Thr Glu Gly Trp Ser Glu Glu Gln Leu Ala Ala Ile Val Thr
 180 185 190
 55 cgt gac agc atg atc ggc acc ggc gtg gtc agc gcg gag gct tcg cga
 624
 Arg Asp Ser Met Ile Gly Thr Gly Val Val Ser Ala Glu Ala Ser Arg
 195 200 205

tga
627

5 <210> 56
 <211> 208
 <212> PRT
 <213> Unknown

10 <220>
 <223> Metagenome - alpha unit nitrile hydratase
 <400> 56

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 1 5 10 15

20 Thr Pro Ile Glu Ala Arg Val Lys Ala Leu Glu Ser Leu Leu Val Ala
 20 25 30

25 Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Ala Ile Ile Asp Thr Tyr
 35 40 45

30 Glu Thr Lys Ile Gly Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala
 50 55 60

35 Ala Val Ala Glu Leu Gly Tyr Gly Gly Arg Gly Gly Glu His Ile Val
 85 90 95

40 Ala Cys Phe Asn Thr Pro Glu Glu His Asn Leu Ile Val Cys Thr Leu
 100 105 110

45 Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Val Trp Tyr
 115 120 125

50 Lys Ser Pro Pro Tyr Arg Ser Lys Ala Val Ile Asp Pro Arg Gly Val
 130 135 140

55 Leu Ala Asp Phe Gly Val Thr Leu Pro Glu Gly Gln Arg Ile Arg Val
 145 150 155 160

60 Trp Asp Ser Thr Ala Glu Thr Arg Phe Ile Val Ile Pro Leu Arg Pro
 165 170 175

65 Ala Gly Thr Glu Gly Trp Ser Glu Glu Gln Leu Ala Ala Ile Val Thr

180 185 190

5 Arg Asp Ser Met Ile Gly Thr Gly Val Val Ser Ala Glu Ala Ser Arg
195 200 205

10 <210> 57
<211> 696
<212> DNA
<213> Unknown

15 <220>
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20 <220>
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<222> (1)..(696)
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48
Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr
1 5 10 15

30 ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac
96
Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His
20 25 30

35 cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc
144
Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu
35 40 45

40 gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac
192
Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
50 55 60

45 gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg
240
Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
65 70 75 80

50 cgc gtt gtc gcg cgg gcc tgg gtt gac ccg gac tac aag caa cgg tta
288
Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
85 90 95

55 ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg
336
Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
100 105 110

cag ggc gct gac atc cgg gtc gtc gaa aac acg gcc act gta cat aac
384
Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn

	115	120	125
	ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc		
	432		
5	Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly		
	130	135	140
	ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat ccg tct cgc gtg gtg		
	480		
10	Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val		
	145	150	155
	atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac		
	528		
15	Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp		
		165	170
			175
	cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta		
	576		
20	His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu		
		180	185
			190
	gtg ctg ccg gag cgg ccg gcc gga acc gaa aac ctg aca gaa gaa gcg		
	624		
25	Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala		
		195	200
			205
	ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc		
	672		
30	Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val		
		210	215
			220
	gcg ccg ccg gga ggc cgc gga tga		
	696		
35	Ala Pro Pro Gly Gly Arg Gly		
		225	230
	<210> 58		
40	<211> 231		
	<212> PRT		
	<213> Unknown		
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	<400> 58		
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			15
	Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His		
		20	25
			30
55	Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu		
		35	40
			45

Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
 50 55 60

5

Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
 65 70 75 80

10

Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
 85 90 95

15

Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
 100 105 110

20

Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn
 115 120 125

Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
 130 135 140

25

Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val
 145 150 155 160

30

Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp
 165 170 175

35

His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
 180 185 190

40

Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
 195 200 205

Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
 210 215 220

45

Ala Pro Pro Gly Gly Arg Gly
 225 230

50

<210> 59
 <211> 609
 <212> DNA
 <213> Unknown

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<222> (1)..(609)

<223>

<400> 59

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 Met Ser Ser Lys Pro Thr Glu Asp Leu Gly Thr Tyr Gln Pro Leu Thr
 1 5 10 15

10 tac tac cag atg atg gaa gtg agc ctg cgc gag ctg ctg gtg gag aag
 96
 Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys
 20 25 30

15 ggc gtg atc acc gaa gcg gaa gtc gcc cgc gcg atg ggc gag atc ggc
 144
 Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly
 35 40 45

20 gcg aga agc ccg gag cgc ggc gcg aag atg gtc gcg cgc gcg tgg gtg
 192
 Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val
 50 55 60

25 gac ccg gcg tac aag gcg cgc atg ctt gcc gac ggc agc aag gcc gcc
 240
 Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala
 65 70 75 80

30 gag gag ctc ggg ttc gag gtg ccg ggc ctc aag ctg atc gtg gtc gag
 288
 Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu
 85 90 95

35 aac acc gcg gac acg cac aac gtg gtc gtg tgc acg ctg tgc tgc tgc
 336
 Asn Thr Ala Asp Thr His Asn Val Val Val Cys Thr Leu Cys Ser Cys
 100 105 110

40 tac ccg cgc atc ctg ctc ggc atc ccg ccc gag tgg tac aag tgc cgc
 384
 Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg
 115 120 125

45 agc tac cgc agc cgc aca gtg cgc gag ccg cgc gcg gtg ctc gcc gaa
 432
 Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu
 130 135 140

50 ttc ggc acg acc atc ccg gag aac gtc gcg atc cga gtg cac gac agc
 480
 Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser
 145 150 155 160

55 act gcg gac atg cgc tac ctc gtg atg ccg atg cgg cct gcg ggc acc
 528
 Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr
 165 170 175

gaa aat ttc acc gaa gag cag ctc gct gca ttg gtg acg cgc gac agc
 576
 Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser
 180 185 190
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 ctg atc ggt gtt tcc tta gca acg ctt ccg tag
 609
 Leu Ile Gly Val Ser Leu Ala Thr Leu Pro
 195 200
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 15 <213> Unknown
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 25 Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys
 20 25 30
 30 Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly
 35 40 45
 35 Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val
 50 55 60
 Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala
 65 70 75 80
 40 Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu
 85 90 95
 45 Asn Thr Ala Asp Thr His Asn Val Val Val Cys Thr Leu Cys Ser Cys
 100 105 110
 50 Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg
 115 120 125
 55 Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu
 130 135 140
 Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser
 145 150 155 160

5 Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr
 165 170 175
 Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser
 180 185 190
 10 Leu Ile Gly Val Ser Leu Ala Thr Leu Pro
 195 200
 15 <210> 61
 <211> 825
 <212> DNA
 <213> Unknown
 20 <220>
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 25 <222> (1)..(825)
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 48
 Met Val Gly Arg Gly Lys Trp Ala Leu Gly Ser Arg Gln Phe Ala Ala
 1 5 10 15
 35 gct gcc aac tgg caa ctt atc agt cgc cct tca tgg tca gct tgt aat
 96
 Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn
 20 25 30
 40 ata ttg gtc ctc atg agc gcc acg cac ccc aaa aag cgc gcc gcc gac
 144
 Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp
 35 40 45
 45 atc ggc ggc aac aaa gcc ggc gcg gtg gac acc gcg gat cac ggc atg
 192
 Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met
 50 55 60
 50 aag ttc tgg gag cgg cag gcc aac gcc ctg cgc acc gcg ctg cgg cgc
 240
 Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg
 65 70 75 80
 55 aat gga ctg atg agc gta gat gag ctg cgc cgc gca gcg gag gac ctg
 288
 Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu
 85 90 95

gga gac cgc tac gcg aag ctt gag tac ttc gag cgc acg acg ttc gcg
 336
 Gly Asp Arg Tyr Ala Lys Leu Glu Tyr Phe Glu Arg Thr Thr Phe Ala
 100 105 110
 5
 ctg cgc acg gtc ctg ctc gaa aag ggc tac ttc acg gag gag tcg ctc
 384
 Leu Arg Thr Val Leu Leu Glu Lys Gly Tyr Phe Thr Glu Glu Ser Leu
 115 120 125
 10
 gcg gcg aag atg gcc gag gtg cgg aag ccg ctt cga tgt gcc gcg caa
 432
 Ala Ala Lys Met Ala Glu Val Arg Lys Pro Leu Arg Cys Ala Ala Gln
 130 135 140
 15
 gaa gga att gcc ggt gaa gaa gaa agt gaa gcg atg aac cca gcg acg
 480
 Glu Gly Ile Ala Gly Glu Glu Glu Ser Glu Ala Met Asn Pro Ala Thr
 145 150 155 160
 20
 ggc aag cag gac ggc caa cgg ctg cca tct acg tat acc gcg gcg ccc
 528
 Gly Lys Gln Asp Gly Gln Arg Leu Pro Ser Thr Tyr Thr Ala Ala Pro
 165 170 175
 25
 ggg cac cga ttc gat gtc ggt gac cgc gtt gtg gtc aag cgc tca aat
 576
 Gly His Arg Phe Asp Val Gly Asp Arg Val Val Val Lys Arg Ser Asn
 180 185 190
 30
 ccg ccc ggc cac cgc cgc acg cct cat tac atc cgc ggc aag acg ggc
 624
 Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly
 195 200 205
 35
 gtg atc gag cgc atc tgc ggc gcc ttc ccc aac ccg gaa gag ctg gca
 672
 Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala
 210 215 220
 40
 tac gga ttc gac ggc gaa ccg aag aag gtg ctc tac cgc gtg cga ttc
 720
 Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe
 225 230 235 240
 45
 cgg caa aaa gag gtg tgg ccg gcc tat cgc ggc ccg gcg cac gac gtg
 768
 Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val
 245 250 255
 50
 atc gag atg gag att ttc gag cat tgg ctc gag ccg gcg cag agc cag
 816
 Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln
 260 265 270
 55
 aaa acc tga
 825
 Lys Thr

5 <210> 62
 <211> 274
 <212> PRT
 <213> Unknown

 10 <220>
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 <400> 62

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 1 5 10 15

 Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn
 20 20 25 30

 20 Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp
 35 40 45

 25 Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met
 50 55 60

 30 Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg
 65 70 75 80

 Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu
 35 85 90 95

 Gly Asp Arg Tyr Ala Lys Leu Glu Tyr Phe Glu Arg Thr Thr Phe Ala
 100 105 110

 40 Leu Arg Thr Val Leu Leu Glu Lys Gly Tyr Phe Thr Glu Glu Ser Leu
 115 120 125

 45 Ala Ala Lys Met Ala Glu Val Arg Lys Pro Leu Arg Cys Ala Ala Gln
 130 135 140

 50 Glu Gly Ile Ala Gly Glu Glu Glu Ser Glu Ala Met Asn Pro Ala Thr
 145 150 155 160

 Gly Lys Gln Asp Gly Gln Arg Leu Pro Ser Thr Tyr Thr Ala Ala Pro
 165 170 175
 55

 Gly His Arg Phe Asp Val Gly Asp Arg Val Val Val Lys Arg Ser Asn
 180 185 190

Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly
 195 200 205
 5 Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala
 210 215 220
 10 Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe
 225 230 235 240
 15 Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val
 245 250 255
 20 Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln
 260 265 270
 Lys Thr
 25 <210> 63
 <211> 627
 <212> DNA
 <213> Unknown
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 35 <220>
 <221> CDS
 <222> (1)..(627)
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 40 <400> 63
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 48
 Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro Val
 1 5 10 15
 45 cgc tac acg atc gac gcg ccc gca ttc cat tcg ccg tgg gaa gtg cgc
 96
 Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg
 20 25 30
 50 gcg aat tcg ctc tat gcg ttc gcg gtg cgc ctc ggc atc ttc aac atg
 144
 Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met
 35 40 45
 55 gac gaa tac cgc cat gcg atc gag cgg atg gag ccg cgc cat tac ctc
 192
 Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu
 50 55 60

ggc gcc ggc tat tac gaa cgc tcg ttg acc ggc ctc gcg acc ttg ctg
 240
 Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu
 65 70 75 80

5

gtc gag aag ggc gtc gtg acg cgc gag gaa ctc gag acc cgg gcg cag
 288
 Val Glu Lys Gly Val Val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln
 85 90 95

10

ggc cgc tac ccg ctg gcg atg ccc agc gcg cct ggc cgc acc aat gcg
 336
 Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala
 100 105 110

15

cag gca cgc gag cgt ttc cag ccg ggc gac cgg gtt cgc gtc aag gcg
 384
 Gln Ala Arg Glu Arg Phe Gln Pro Gly Asp Arg Val Arg Val Lys Ala
 115 120 125

20

gat ttc gtg tcg ggg cac gtg cgg atg ccg gcg tac atc cgc ggc aag
 432
 Asp Phe Val Ser Gly His Val Arg Met Pro Ala Tyr Ile Arg Gly Lys
 130 135 140

25

acc ggc gtg gtc gtc agc gag tcc ccg gac tat ccg ttt ccc gat gcg
 480
 Thr Gly Val Val Val Ser Glu Ser Pro Asp Tyr Pro Phe Pro Asp Ala
 145 150 155 160

30

cat gcg cac tcg gtc gat gcc cag gac gag cca acc tac gac gtg cgc
 528
 His Ala His Ser Val Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val Arg
 165 170 175

35

ttc cgc agc gag gat cta tgg ccg gat tcc gcc gat tcc gca ctc gtt
 576
 Phe Arg Ser Glu Asp Leu Trp Pro Asp Ser Ala Asp Ser Ala Leu Val
 180 185 190

40

cac gtc ggc gta ttc cag agc tac ctc gag cgg gag tcg acg cca gga
 624
 His Val Gly Val Phe Gln Ser Tyr Leu Glu Arg Glu Ser Thr Pro Gly
 195 200 205

45

tag
 627

50

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 <212> PRT
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 <400> 64

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 5 Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg
 20 25 30
 10 Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met
 35 40 45
 Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu
 50 55 60
 15 Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu
 65 70 75 80
 20 Val Glu Lys Gly Val Val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln
 85 90 95
 25 Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala
 100 105 110
 30 Gln Ala Arg Glu Arg Phe Gln Pro Gly Asp Arg Val Arg Val Lys Ala
 115 120 125
 Asp Phe Val Ser Gly His Val Arg Met Pro Ala Tyr Ile Arg Gly Lys
 130 135 140
 35 Thr Gly Val Val Val Ser Glu Ser Pro Asp Tyr Pro Phe Pro Asp Ala
 145 150 155 160
 40 His Ala His Ser Val Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val Arg
 165 170 175
 45 Phe Arg Ser Glu Asp Leu Trp Pro Asp Ser Ala Asp Ser Ala Leu Val
 180 185 190
 50 His Val Gly Val Phe Gln Ser Tyr Leu Glu Arg Glu Ser Thr Pro Gly
 195 200 205
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 55 <212> DNA
 <213> Unknown
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 <222> (1)..(660)
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 10 Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile
 1 5 10 15

cgc cgc gag gag aac gag ccc gct ttc cac gag ccc tgg gag ggg cgg
 96
 15 Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg
 20 25 30

gtt ttc gct ctg acc acg gcg gtc gag gcc tgg ggt cgg tgg acc ctg
 144
 20 Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu
 35 40 45

gat gct tcc cga cac cgg atc gag cgg atg aat gcg gcg gac tat ctg
 192
 25 Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu
 50 55 60

cgg gtg agc tat tac gag aag tgg ctc gag tcg ctt ctc gct ctc ctg
 240
 30 Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu
 65 70 75 80

tcc gag acc gga atg gcg agt ccg gcg gag ata cgg agt ggg gag cgt
 288
 35 Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg
 85 90 95

gcc gac ggc aca ccg aaa gcg acc ccg ccg ctc ccg gcc gac cac gtg
 336
 40 Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val
 100 105 110

acg gcg att ctc gcc agc ggg ttt ccc gcg agc cgg gag gcg gga gct
 384
 45 Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala
 115 120 125

gcg cct cgc ttc cga gtg agc gag cgg gtg cgc acc cgg aac atc aac
 432
 50 Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn
 130 135 140

ccg acg act cac acg cgc ctt ccg cga tac gcc cgg cgg aag ctc ggg
 480
 55 Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly
 145 150 155 160

acg atc gag cgc gac cac gga gtg ttc gtc ttc ccg gat acg aac gcg
 528

Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala
 165 170 175
 5 cac gct ctc ggg gag aaa ccg cag cac gtc tat tcg gtt cgt ttc gag
 576
 His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu
 180 185 190
 10 gcg cgt gag ctc tgg ggc gag act gcc agg cca gag gat tcc gtc tac
 624
 Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr
 195 200 205
 15 atc gat ctt tgg gac gag tac ctt gaa ccc gtg tag
 660
 Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val
 210 215
 20 <210> 66
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 25 <220>
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 <400> 66
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 35 Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg
 20 25 30
 Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu
 35 40 45
 40 Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu
 50 55 60
 45 Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu
 65 70 75 80
 50 Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg
 85 90 95
 55 Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val
 100 105 110
 Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala
 115 120 125

	Ala	Pro	Arg	Phe	Arg	Val	Ser	Glu	Arg	Val	Arg	Thr	Arg	Asn	Ile	Asn
	130						135					140				
5																
	Pro	Thr	Thr	His	Thr	Arg	Leu	Pro	Arg	Tyr	Ala	Arg	Arg	Lys	Leu	Gly
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10																
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					165					170					175	
15																
	His	Ala	Leu	Gly	Glu	Lys	Pro	Gln	His	Val	Tyr	Ser	Val	Arg	Phe	Glu
				180					185					190		
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	Ala	Arg	Glu	Leu	Trp	Gly	Glu	Thr	Ala	Arg	Pro	Glu	Asp	Ser	Val	Tyr
			195					200					205			
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	1				5				10					15		
50																
	gtc	gag	ccc	gag	cgc	aac	gag	cgc	cgc	ttt	cac	cag	cgc	tgg	gag	ggc
	96															
	Val	Glu	Pro	Glu	Pro	Asn	Glu	Pro	Pro	Phe	His	Gln	Arg	Trp	Glu	Gly
				20				25					30			
55																
	cgg	gtg	ctg	ggg	atg	cag	cgc	gcc	atg	ggc	ttt	acc	ggg	ctg	tgg	acc
	144															
	Arg	Val	Leu	Gly												

	ctg ggt tgc tcc tac tat cgg cgc tgg ttt ctt ggc ctg gag agc cgg
	240
5	Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg 65 70 75 80
	ctg ctg ctg cgc gcc ctc gtt ggc gag gac gag atc gcg gca gcc cgt
	288
10	Leu Leu Leu Arg Gly Leu Val Gly Glu Asp Glu Ile Ala Ala Gly Arg 85 90 95
	tgc atg cgc gcc gcc ggc gcc atg ttg ccg cgc acc ctg acc cag gcc gat
	336
15	Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp 100 105 110
	gtg gag aaa acc ctg acc cgc gcc gac ttc gcc cgc ccg acc aac acc
	384
20	Val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr 115 120 125
	ccg gcg cgt ttc cag ccg gcc gac cgg gtg caa acg aag aac atc aac
	432
25	Pro Ala Arg Phe Gln Pro Gly Asp Arg Val Gln Thr Lys Asn Ile Asn 130 135 140
	ccg gcg acc cac acc cgc ctg ccg cgc tat gcc cgc gcc aag act gcc
	480
30	Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly 145 150 155 160
	acg gtc gag gcg gtc cgc gcc gtt cac gtc ttt ccc gac acc gcc gcg
	528
35	Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala 165 170 175
	ctc gcc gcc gcc gac gac ccg caa tgg ctc tac gcc gtg gtc ttc ccg
	576
40	Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val Val Phe Pro 180 185 190
	gcg cgc gag ttg tgg gga gag gcg gcc gat ccc gcg atc aaa atc tcg
	624
45	Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser 195 200 205
	atc gag gcg ttc gaa ccc tat atc gac ccc gca tga
	660
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	<211> 219
55	<212> PRT
	<213> Unknown
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20 25 30

10 Arg Val Leu Gly Met Gln Arg Ala Met Gly Phe Thr Gly Leu Trp Thr
35 40 45

15 Ile Asp Ala Gly Arg Ala Ser Leu Glu Ala Leu Pro Pro Leu Ala Tyr
50 55 60

20 Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg
65 70 75 80

25 Leu Leu Leu Arg Gly Leu Val Gly Glu Asp Glu Ile Ala Ala Gly Arg
85 90 95

Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp
100 105 110

30 Val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr
115 120 125

35 Pro Ala Arg Phe Gln Pro Gly Asp Arg Val Gln Thr Lys Asn Ile Asn
130 135 140

40 Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly
145 150 155 160

45 Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala
165 170 175

Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val Val Phe Pro
180 185 190

50 Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser
195 200 205

55 Ile Glu Ala Phe Glu Pro Tyr Ile Asp Pro Ala
210 215

<210> 69
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 <212> DNA
 <213> Unknown

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 20 gag ccg gaa gcg aac gag ccc gcc ttc cat gcg gaa tgg gaa ggc cgc
 96
 Glu Pro Glu Ala Asn Glu Pro Ala Phe His Ala Glu Trp Glu Gly Arg
 20 25 30
 25 tgc ctc gcg ctc aac cgc gcc atg ggt gcg atc ggc gcc tgg acc atc
 144
 Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile
 35 40 45
 30 gat gaa ggc cgt gcc ggc atc gag atc ctg ccg ccg gag att tat ctt
 192
 Asp Glu Gly Arg Ala Gly Ile Glu Ile Leu Pro Pro Glu Ile Tyr Leu
 50 55 60
 35 ggc agt tcg tac tat gga aaa tgg gcg cgg cgg ctg gag aat atg gtg
 240
 Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val
 65 70 75 80
 40 gtc gca cgc ggg ttc gcg ggc gcc gat gaa ctc gcc gcg ggt cgc gca
 288
 Val Ala Arg Gly Phe Ala Gly Ala Asp Glu Leu Ala Ala Gly Arg Ala
 85 90 95
 45 gcg cgt ccc ggc aga tcg gtg aaa cga aag ctt acg gtc gcc gaa gtg
 336
 Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val
 100 105 110
 50 ccg cgc acg ctg acg cgc ggt tca ttt ttc cgc gag gca aca aag ccg
 384
 Pro Arg Thr Leu Thr Arg Gly Ser Phe Phe Arg Glu Ala Thr Lys Pro
 115 120 125
 55 gca cga ttt gcg gtc ggc gaa cgc gtg cgc acc agg aac att cat ccg
 432
 Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro
 130 135 140

gcg acg cac act cgg ttg ccg cga tat gcg cgc ggc cat gtc ggc gtg
 480
 Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly His Val Gly Val
 145 150 155 160
 5 atc gag gcg atc cgc ggt tgc cac gta ttt ccc gac tcg gtt gcg atc
 528
 Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile
 165 170 175
 10 ggc gcc ggc gag aac ccg caa tgg ctt tat acg gtg gtg ttc gaa ggc
 576
 Gly Ala Gly Glu Asn Pro Gln Trp Leu Tyr Thr Val Val Phe Glu Gly
 180 185 190
 15 cgc acg ctg tgg ggc gat agc gcc gat ccg acg ctt aag gtc tcg atc
 624
 Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile
 195 200 205
 20 gag gcg ttc gag ccg tat ctg gaa ccg gcc caa cca tga
 663
 Glu Ala Phe Glu Pro Tyr Leu Glu Pro Ala Gln Pro
 210 215 220
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 <210> 70
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 30 <213> Unknown
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 20 25 30
 45 Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile
 35 40 45
 50 Asp Glu Gly Arg Ala Gly Ile Glu Ile Leu Pro Pro Glu Ile Tyr Leu
 50 55 60
 55 Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val
 65 70 75 80
 Val Ala Arg Gly Phe Ala Gly Ala Asp Glu Leu Ala Ala Gly Arg Ala
 85 90 95

Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val
100 105 110

5 Pro Arg Thr Leu Thr Arg Gly Ser Phe Phe Arg Glu Ala Thr Lys Pro
115 120 125

10 Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro
130 135 140

15 Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly His Val Gly Val
145 150 155 160

20 Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile
165 170 175

Gly Ala Gly Glu Asn Pro Gln Trp Leu Tyr Thr Val Val Phe Glu Gly
180 185 190

25 Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile
195 200 205

30 Glu Ala Phe Glu Pro Tyr Leu Glu Pro Ala Gln Pro
210 215 220

35 <210> 71
<211> 888
<212> DNA
<213> Unknown

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<222> (1)..(888)

45 <223>

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50 Met Asn Gly Val His Asp Leu Gly Gly Met Asp Gly Phe Gly Arg Val
1 5 10 15

atg gcg gag gcg gac gag ccg gtc ttt cat gag ccc tgg gaa ggt cgc
96
55 Met Ala Glu Ala Asp Glu Pro Val Phe His Glu Pro Trp Glu Gly Arg
20 25 30

gtg ttt gcg ctc aac atg ctc ggc atc ggg cgc gag ccc att ccg gtg
144

Val Phe Ala Leu Asn Met Leu Gly Ile Gly Arg Glu Pro Ile Pro Val
 35 40 45
 5 gac gcg ctg cgc cat cgc att gag cgg atc gag ccg tgg cgc tat ctg
 192
 Asp Ala Leu Arg His Arg Ile Glu Arg Ile Glu Pro Trp Arg Tyr Leu
 50 55 60
 10 acg tcg agc tat tac gaa cga tgg ctg gcc gaa atg gag cag gcc atc
 240
 Thr Ser Ser Tyr Tyr Glu Arg Trp Leu Ala Glu Met Glu Gln Ala Ile
 65 70 75 80
 15 atc gat gcg ggc acg ctg act cct ggt gaa atc gat gcg cga atg ggc
 288
 Ile Asp Ala Gly Thr Leu Thr Pro Gly Glu Ile Asp Ala Arg Met Gly
 85 90 95
 20 gag ctc gaa acg gat cct gat cgc cca ctg cca agg act gat aac cct
 336
 Glu Leu Glu Thr Asp Pro Asp Arg Pro Leu Pro Arg Thr Asp Asn Pro
 100 105 110
 25 gag cat gcc gat ggg gtg gcg gcg gcg ttg cgc gcc ggc agt ccc gta
 384
 Glu His Ala Asp Gly Val Ala Ala Ala Leu Arg Ala Gly Ser Pro Val
 115 120 125
 30 acg cgc aag att cgc aag cag ccg cgc ttc aca atc ggc gat cgg gtc
 432
 Thr Arg Lys Ile Arg Lys Gln Pro Arg Phe Thr Ile Gly Asp Arg Val
 130 135 140
 35 gta acg cgc aat ctt aat ccg cac ggc cat acg cgg ctg ccg cgc tat
 480
 Val Thr Arg Asn Leu Asn Pro His Gly His Thr Arg Leu Pro Arg Tyr
 145 150 155 160
 40 gcg cgc ggc aag cgc ggc gtc gta acg ctg cac cat ggc gca cat gtc
 528
 Ala Arg Gly Lys Arg Gly Val Val Thr Leu His His Gly Ala His Val
 165 170 175
 45 ttt ccg gat acg aac gcg cac ggg ctg ggc gag cat ccg cag cat ctc
 576
 Phe Pro Asp Thr Asn Ala His Gly Leu Gly Glu His Pro Gln His Leu
 180 185 190
 50 tat acg gtg cga ttt cct gcg cgc gag tta tgg agc gac gcg gcc gag
 624
 Tyr Thr Val Arg Phe Pro Ala Arg Glu Leu Trp Ser Asp Ala Ala Glu
 195 200 205
 55 ccg aaa gaa tcg ata atg atc gat ttg tgg gag agc tat ctt caa ccc
 672
 Pro Lys Glu Ser Ile Met Ile Asp Leu Trp Glu Ser Tyr Leu Gln Pro
 210 215 220

gat atc ggc agc aaa gcg tcg tcg tcc gcg aaa ggc aaa gcg acg ccg
 720
 Asp Ile Gly Ser Lys Ala Ser Ser Ser Ala Lys Gly Lys Ala Thr Pro
 225 230 235 240
 5
 aaa gtt aag ccc gca atg gcc aag gca acc gcc aag gta agc gtc tcg
 768
 Lys Val Lys Pro Ala Met Ala Lys Ala Thr Ala Lys Val Ser Val Ser
 245 250 255
 10
 gcc aag gcc aaa act cgg gga aag gcg gcg ccg aag gag cgt cca aaa
 816
 Ala Lys Ala Lys Thr Arg Gly Lys Ala Ala Pro Lys Glu Arg Pro Lys
 260 265 270
 15
 ctg aaa cct gcg cga gcg gcg acc tca gca gca tcc ggc ggc gaa aaa
 864
 Leu Lys Pro Ala Arg Ala Ala Thr Ser Ala Ala Ser Gly Gly Glu Lys
 275 280 285
 20
 gct aag cga aag gcc aaa cga tga
 888
 Ala Lys Arg Lys Ala Lys Arg
 290 295
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 <211> 295
 <212> PRT
 30 <213> Unknown
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 Met Ala Glu Ala Asp Glu Pro Val Phe His Glu Pro Trp Glu Gly Arg
 20 25 30
 45
 Val Phe Ala Leu Asn Met Leu Gly Ile Gly Arg Glu Pro Ile Pro Val
 35 40 45
 50
 Asp Ala Leu Arg His Arg Ile Glu Arg Ile Glu Pro Trp Arg Tyr Leu
 50 55 60
 55
 Thr Ser Ser Tyr Tyr Glu Arg Trp Leu Ala Glu Met Glu Gln Ala Ile
 65 70 75 80
 Ile Asp Ala Gly Thr Leu Thr Pro Gly Glu Ile Asp Ala Arg Met Gly
 85 90 95

Glu Leu Glu Thr Asp Pro Asp Arg Pro Leu Pro Arg Thr Asp Asn Pro
 100 105 110
 5
 Glu His Ala Asp Gly Val Ala Ala Leu Arg Ala Gly Ser Pro Val
 115 120 125
 10
 Thr Arg Lys Ile Arg Lys Gln Pro Arg Phe Thr Ile Gly Asp Arg Val
 130 135 140
 15
 Val Thr Arg Asn Leu Asn Pro His Gly His Thr Arg Leu Pro Arg Tyr
 145 150 155 160
 20
 Ala Arg Gly Lys Arg Gly Val Val Thr Leu His His Gly Ala His Val
 165 170 175
 Phe Pro Asp Thr Asn Ala His Gly Leu Gly Glu His Pro Gln His Leu
 180 185 190
 25
 Tyr Thr Val Arg Phe Pro Ala Arg Glu Leu Trp Ser Asp Ala Ala Glu
 195 200 205
 30
 Pro Lys Glu Ser Ile Met Ile Asp Leu Trp Glu Ser Tyr Leu Gln Pro
 210 215 220
 35
 Asp Ile Gly Ser Lys Ala Ser Ser Ser Ala Lys Gly Lys Ala Thr Pro
 225 230 235 240
 40
 Lys Val Lys Pro Ala Met Ala Lys Ala Thr Ala Lys Val Ser Val Ser
 245 250 255
 45
 Ala Lys Ala Lys Thr Arg Gly Lys Ala Ala Pro Lys Glu Arg Pro Lys
 260 265 270
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 Leu Lys Pro Ala Arg Ala Ala Thr Ser Ala Ala Ser Gly Gly Glu Lys
 275 280 285
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 Ala Lys Arg Lys Ala Lys Arg
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 <211> 630
 <212> DNA
 <213> Unknown
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48
Met Asp Gly Ile His Asp Leu Gly Gly Met Ser Gly Phe Gly Leu Val
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15 gag atc gag ccc gat gag ccg gtg ttc cac gag ccc tgg gag gcg ctg
96
Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu
20 25 30
20 gtt ttc gct ctg atg act ctc ggt atc ggg aag ctc ggc gcg tac aac
144
Val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn
35 40 45
25 gcc gat gag tac cgc cac tcg atc gag cgg atg gat ccg gcc cac tac
192
Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr
50 55 60
30 ctt gcg gcg acg tac tac gag cgc atg ctc acc ggc gtc gca acg ctc
240
Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu
65 70 75 80
35 ctc gtc gag aag aac gtc gtt gcc cgc gac gag ctc gaa gcg cgc gcc
288
Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala
85 90 95
40 ggc ggg ccc ttc ccg ctg tca cgg ccg gtg gcc gag cgg ccg acg gcg
336
Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala
100 105 110
45 gac ctt cgg ccc cag cca caa cca cgc ttc gcg gtc ggg gat cgg gtc
384
Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val
115 120 125
50 gtc gtg cgc gac atc cac ccg gcc ggg cat act cgt gtg ccg cgc tac
432
Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr
130 135 140
55 gtg cgg ggc aag cgc ggg acc gtc gtg cac gtc gcg ccg aaa ttc tcg
480
Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser
145 150 155 160

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ttc ccc gac acg gcc gcg cac ggg ctg acc cat cgg agc gag cac acg
 528
 Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr
 165 170 175
 5
 tat cac gtg gaa ttc gtc gcg agt gac ctt tgg gcc gac gtg gcc ggg
 576
 Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly
 180 185 190
 10
 agc aat gag agc gta ctc gtg gac ctg tgg gac ggc tat ctg gag ggc
 624
 Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly
 195 200 205
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 gca tga
 630
 Ala
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 Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu
 20 25 30
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 Val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn
 35 40 45
 45
 Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr
 50 55 60
 50
 Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu
 65 70 75 80
 Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala
 85 90 95
 55
 Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala
 100 105 110

Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val
 115 120 125

5 Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr
 130 135 140

10 Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser
 145 150 155 160

15 Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr
 165 170 175

Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly
 180 185 190

20 Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly
 195 200 205

25 Ala

30 <210> 75
 <211> 651
 <212> DNA
 <213> Unknown

35 <220>
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45 Met Arg Gly Thr His Asp Leu Gly Gly Leu Pro Ala Gly Pro Val Asp
 1 5 10 15

acc gct ccc cac gaa ccg acc ttc tgg gaa aag cag gtg gac gcg atc
 96

50 Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile
 20 25 30

cac ggc ctg ctc ggc gat tcc aag cgc cgc atc acg ctg cgc gac gag
 144

55 His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu
 35 40 45

aac cgc ctc tat atc gaa tcg ctc ggc gac gac gtc tac aac acg ctc
 192

Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu
 50 55 60

5 ggc tat tac gag cgc tgg acc gcc gcc atg tgc cgc cag ctc atc gac
 240
 Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp
 65 70 75 80

10 aag ggc gtg ctg acg cag gac gag atc gac gcc aag atc gcc gag ctg
 288
 Lys Gly Val Leu Thr Gln Asp Glu Ile Asp Ala Lys Ile Ala Glu Leu
 85 90 95

15 cgc gcc cgc ggc gtc ggc gcg gga cga cga aac ggc ctg caa acc
 336
 Arg Ala Arg Gly Val Gly Ala Gly Arg Arg Arg Asn Gly Leu Gln Thr
 100 105 110

20 gtg agc gcc gat ctg gcc gcc gat ctg gcc atc gcg ccg cgc ttc gcc
 384
 Val Ser Ala Asp Leu Ala Ala Asp Leu Ala Ile Ala Pro Arg Phe Ala
 115 120 125

25 gcc ggc gac cgc gtg cgg gtg cgc gac gat tat ccg ccc ggg cac atc
 432
 Ala Gly Asp Arg Val Arg Val Arg Asp Asp Tyr Pro Pro Gly His Ile
 130 135 140

30 cgc acg ccg gtc tat gtg cgc ggc aag acg ggc gtg gtg acg cgc tgc
 480
 Arg Thr Pro Val Tyr Val Arg Gly Lys Thr Gly Val Val Thr Arg Cys
 145 150 155 160

35 ttc ggc gcg ttc aag aac ccg gaa ttg ctc gcc atc ggc aag gac ggc
 528
 Phe Gly Ala Phe Lys Asn Pro Glu Leu Leu Ala Ile Gly Lys Asp Gly
 165 170 175

40 ctg ccc aag aaa att ctc tac gaa gtg cgc ttc aag cag acc gat ctc
 576
 Leu Pro Lys Lys Ile Leu Tyr Glu Val Arg Phe Lys Gln Thr Asp Leu
 180 185 190

45 tgg ccc gac tat gcc ggg ccg gcg acc gat acg ctg ctg atc gac atc
 624
 Trp Pro Asp Tyr Ala Gly Pro Ala Thr Asp Thr Leu Leu Ile Asp Ile
 195 200 205

50 tac gaa cat tgg ctg agc gac gcg tga
 651
 Tyr Glu His Trp Leu Ser Asp Ala
 210 215

55 <210> 76
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<400> 76

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10 Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile
20 25 30

15 His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu
35 40 45

Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu
50 55 60

20 Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp
65 70 75 80

25 Lys Gly Val Leu Thr Gln Asp Glu Ile Asp Ala Lys Ile Ala Glu Leu
85 90 95

30 Arg Ala Arg Gly Val Gly Ala Gly Arg Arg Arg Asn Gly Leu Gln Thr
100 105 110

35 Val Ser Ala Asp Leu Ala Ala Asp Leu Ala Ile Ala Pro Arg Phe Ala
115 120 125

Ala Gly Asp Arg Val Arg Val Arg Asp Asp Tyr Pro Pro Gly His Ile
130 135 140

40 Arg Thr Pro Val Tyr Val Arg Gly Lys Thr Gly Val Val Thr Arg Cys
145 150 155 160

45 Phe Gly Ala Phe Lys Asn Pro Glu Leu Leu Ala Ile Gly Lys Asp Gly
165 170 175

50 Leu Pro Lys Lys Ile Leu Tyr Glu Val Arg Phe Lys Gln Thr Asp Leu
180 185 190

55 Trp Pro Asp Tyr Ala Gly Pro Ala Thr Asp Thr Leu Leu Ile Asp Ile
195 200 205

Tyr Glu His Trp Leu Ser Asp Ala
210 215

5 <210> 77
 <211> 657
 <212> DNA
 <213> Unknown

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 1 5 10 15

25 cag atc gag aag gac gag tcg ccc ttc cat gcg cgc tgg gaa ggc cgg
 96
 Gln Ile Glu Lys Asp Glu Ser Pro Phe His Ala Arg Trp Glu Gly Arg
 20 25 30

30 gcg caa gcg atg tac aac gcc att gcg gcc acg ggc aga ctg gtg ctt
 144
 Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu
 35 40 45

35 ggc ggt aga ccc aca cgg gaa ggg ttc ccg ccg gcc gaa tat ctc cgc
 192
 Gly Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg
 50 55 60

40 atg agc tac tat gaa ttg ggt ttc agg gtg ctg gtc gag gac ttg gtc
 240
 Met Ser Tyr Tyr Glu Leu Gly Phe Arg Val Leu Val Glu Asp Leu Val
 65 70 75 80

45 ctg aac ggt ttg gtg acg cgc gcg gaa atc acg agc ggc cgt ccg gca
 288
 Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala
 85 90 95

50 aag ggg gct gca aag tcg acg ccc gca atc acc gcc gcc acc gcg cag
 336
 Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln
 100 105 110

55 gca tat atg ttc gcg ctc aaa tcg acc cgg cga gac gta ccg gtc acg
 384
 Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr
 115 120 125

gcg cgt ttc caa gtc ggt cag cgt gtg cgc gcg cgc aac atc aat ccg
 432
 Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro

130 135 140
 gtc acc cat acg cgc ctg ccc cgt tac gcg cgc ggc aaa ttc ggc gtt
 480
 5 Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val
 145 150 155 160
 atc gaa cgt gac cac ggt gtt tac agg ttc gac gat tcc ttt gcc acg
 528
 10 Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr
 165 170 175
 tcc ggc gac gag aag ccc cag cac gtt tat tct gtg cgc ttc gcg gcg
 576
 15 Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala
 180 185 190
 cgc gaa cta tgg ggc gaa gcc gcg ccg ccg cga gat gct gtc tat atc
 624
 20 Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile
 195 200 205
 gaa atc tgg gat gac aac ctt gag cca gcg tga
 657
 25 Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala
 210 215
 <210> 78
 30 <211> 218
 <212> PRT
 <213> Unknown
 <220>
 35 <223> Metagenome - beta unit nitrile hydratase - M50bD9
 <400> 78
 Met Asn Gly Met His Asp Met Gly Gly Met His Gly Met Gly Pro Ile
 40 1 5 10 15
 Gln Ile Glu Lys Asp Glu Ser Pro Phe His Ala Arg Trp Glu Gly Arg
 20 25 30
 45 Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu
 35 40 45
 50 Gly Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg
 50 55 60
 55 Met Ser Tyr Tyr Glu Leu Gly Phe Arg Val Leu Val Glu Asp Leu Val
 65 70 75 80
 Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala

	85	90	95
5	Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln 100 105 110		
10	Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr 115 120 125		
15	Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro 130 135 140		
20	Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val 145 150 155 160		
25	Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr 165 170 175		
30	Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala 180 185 190		
35	Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile 195 200 205		
40	Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala 210 215		
45	<210> 79 <211> 696 <212> DNA <213> Unknown		
50	<220> <223> Metagenome - beta unit nitrile hydratase - M3aG10		
55	<220> <221> CDS <222> (1)..(696) <223>		
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65	ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac 96 Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His 20 25 30		

5 cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc
 144
 Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu
 35 40 45
 10 gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac
 192
 Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
 50 55 60
 15 gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg
 240
 Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
 65 70 75 80
 20 cgc gtt gtc gcg cgg gcc tgg gtt gac ccg gac tac aag caa cgg tta
 288
 Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
 85 90 95
 25 ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg
 336
 Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
 100 105 110
 30 cag ggc gct gac atc cgg gtc gtc gaa aac acg gcc act gta cat aac
 384
 Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn
 115 120 125
 35 ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc
 432
 Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
 130 135 140
 40 ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg
 480
 Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val
 145 150 155 160
 45 atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac
 528
 Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp
 165 170 175
 50 cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta
 576
 His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
 180 185 190
 55 gtg ctg ccg gag cgg ccg gcc gga acc gaa aac ctg aca gaa gaa gcg
 624
 Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
 195 200 205
 60 ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc
 672
 Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
 210 215 220

gcg ccg ccg gga ggc cgc gga tga
 696
 Ala Pro Pro Gly Gly Arg Gly
 5 225 230

<210> 80
 <211> 231
 10 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M3aG10
 15 <400> 80

Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr
 1 5 10 15
 20

Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His
 20 25 30
 25

Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu
 35 40 45
 30

Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp
 50 55 60
 35

Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala
 65 70 75 80
 40

Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu
 85 90 95
 45

Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser
 100 105 110
 50

Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn
 115 120 125
 55

Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
 130 135 140
 60

Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val
 145 150 155 160
 65

Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp
 165 170 175

5 His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
 180 185 190

Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
 195 200 205

10 Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
 210 215 220

15 Ala Pro Pro Gly Gly Arg Gly
 225 230

20 <210> 81
 <211> 327
 <212> DNA
 <213> Unknown

25 <220>
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30 <220>
 <221> CDS
 <222> (1)..(327)
 <223>

<400> 81
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 48

35 Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe
 1 5 10 15

gcg ttg gcg atc tcg ttg caa gac cgt ggc gtg ttc acg cga gac gaa
 96

40 Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu
 20 25 30

tgg gcg gcg gca ctc ggc gat gaa atc aag aag gcg caa gct gcc ggc
 144

45 Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly
 35 40 45

gat ccc gat acg ggc gag act tat tac cat cat tgg atg gca gcg ctc
 192

50 Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu
 50 55 60

gaa cgg ctg att gca gcc aag ggt gtt gcc gat acg cag acg ctc gcg
 240

55 Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala
 65 70 75 80

cgc aca cgc gac gcc tgg cag cac gcc tgt gcg cga acg ccg cat ggc
 288

Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly
 85 90 95
 5 gcg cca atc gag cta aga ccg gac gac ttc agg aat tga
 327
 Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn
 100 105
 10 <210> 82
 <211> 108
 <212> PRT
 <213> Unknown
 15 <220>
 <223> Metagenome - p12K unit
 <400> 82
 20 Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe
 1 5 10 15
 25 Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu
 20 25 30
 30 Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly
 35 40 45
 Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu
 50 55 60
 35 Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala
 65 70 75 80
 40 Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly
 85 90 95
 45 Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn
 100 105
 50 <210> 83
 <211> 321
 <212> DNA
 <213> Unknown
 <220>
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 55 <220>
 <221> CDS
 <222> (1)..(321)
 <223>

<400> 83
 atg aga aca gtt gct gag caa atc gcg gct gat ctt gcg agt ccg gcg
 48
 5 Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala
 1 5 10 15

 gcg att ccg cgc cgc aac ggc gag ccg gtc ttc gac gag cct tgg gaa
 96
 10 Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu
 20 25 30

 agt cgt gcg ttt ggg ata gcg gtc gcc ctt tcc gag ggt ggc ctc tat
 144
 15 Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr
 35 40 45

 tca tgg gat gaa ttt cgc gat tgc ctg att gct gaa atc aca gcg gcg
 192
 20 Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala
 50 55 60

 gat gcg cgc ggc gag cat acg agc tat tac gaa cgg ttt ctc gcc gcc
 240
 25 Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala
 65 70 75 80

 ctg cag cat ctg ctc gcg gcc aaa cgc ctc tgc act ccc gat gaa gtc
 288
 30 Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val
 85 90 95

 gag cgg cgg atg aac act agc gca ggc acc tga
 321
 35 Glu Arg Arg Met Asn Thr Ser Ala Gly Thr
 100 105

 <210> 84
 40 <211> 106
 <212> PRT
 <213> Unknown

 <220>
 45 <223> Metagenome - p12K unit

 <400> 84

 Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala
 50 1 5 10 15

 Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu
 20 25 30
 55

 Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr
 35 40 45

Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala
 50 55 60

5 Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala
 65 70 75 80

10 Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val
 85 90 95

15 Glu Arg Arg Met Asn Thr Ser Ala Gly Thr
 100 105

20 <210> 85
 <211> 426
 <212> DNA
 <213> Unknown

25 <220>
 <223> Metagenome - p12K unit

30 <220>
 <221> CDS
 <222> (1)..(426)
 <223>

35 atg aca acc ttg agc cag cgt gaa gcg gcc ccc tcg gcc gag ctt ctt
 48
 Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu
 1 5 10 15

40 gac cta ccg caa ctt cca agc gac acc gac ggc ccc gtc ttc gcg gaa
 96
 Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu
 20 25 30

45 cct tgg gaa gcg gaa gcg ttt gcg ctt gcc gta agt ctt tca gag caa
 144
 Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln
 35 40 45

50 gga cat ttc acg tgg aag gaa tgg gca gca acg ctc gcc gat gaa ctg
 192
 Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu
 50 55 60

55 gag ggc gcc gcc aat cgc ggc gag ccg gat gac ggt acg cat tat tat
 240
 Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr
 65 70 75 80

gag tac tgg ctg acg gcc ctg gaa agg ctg gtt acg atc aag ggc ctg
 288
 Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu

	85	90	95
	aca gat cag caa gcg atg cgc gag cgc aaa gag gcg tgg gaa gaa gcc		
	336		
5	Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala	105	110
	100		
	tat cgc cat acc ccg cat ggc gcg cca gtt gaa ctt atg tct ccg ctc		
	384		
10	Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu	120	125
	115		
	gat caa agc cgg ata gcc gaa gag gac agc gaa tcc tca tag		
	426		
15	Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser	135	140
	130		
20	<210> 86		
	<211> 141		
	<212> PRT		
	<213> Unknown		
25	<220>		
	<223> Metagenome - p12K unit		
	<400> 86		
30	Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu	10	15
	1	5	
	Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu	25	30
	20		
35	Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln	40	45
	35		
40	Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu	55	60
	50		
45	Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr	70	75
	65		80
50	Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu	85	90
	85		95
55	Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala	105	110
	100		
	Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu	120	125
	115		

Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser
130 135 140